

# The role of migration in the evolution of phenotypic switching

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## Supplementary Material

Consider an infinite, haploid population divided spatially into two demes,  $E_x$  and  $E_y$ . Each individual in the population is defined by two biallelic loci: a major locus  $A/a$  which controls the phenotype and thus the fitness of the individual, and a modifier locus  $M/m$  which controls the switching rate between phenotypes  $A$  and  $a$ . Switching occurs only at the phenotypic locus, at a rate that is assumed to be the same in both directions. Selection acts only on the phenotypes  $A$  and  $a$ . The modifier locus  $M/m$  is assumed to be selectively neutral.

Within each deme, the environment varies temporally between two states,  $T_1$  and  $T_2$ . At each time-step, individuals first experience selection, followed by switching, recombination, and finally migration. The recursions representing the change in frequency at each generation are presented below.

### Equations describing the change in frequency at every generation.

Denote by  $x_1, x_2, x_3, x_4$  the frequencies of  $MA, Ma, mA$ , and  $ma$  in deme  $E_x$  and let  $y_1, y_2, y_3$ , and  $y_4$  be the analogous frequencies in deme  $E_y$ .

The fitness of phenotype  $i$  in temporal state  $j$  within deme  $l$  is denoted by  $w_{i,jl}$  ( $i$  in  $\{A, a\}$ ,  $j$  in  $\{1, 2\}$ ,  $l$  in  $\{x, y\}$ ). The mean fitness in deme  $l$  is denoted by  $\bar{w}_l$ ,  $l \in \{x, y\}$ . After selection, there is a process of switching between phenotypic states. There are two possible switching rates:  $\mu_M$ , associated with allele  $M$  and  $\mu_m$  associated with allele  $m$ . After selection and switching, the equations for the frequencies of

the four genotypes in the two demes are

$$\begin{aligned}
\tilde{x}_1 &= (1 - \mu_M) \frac{w_{A,jx}}{\bar{w}_x} x_1 + \mu_M \frac{w_{a,jx}}{\bar{w}_x} x_2 \\
\tilde{x}_2 &= \mu_M \frac{w_{A,jx}}{\bar{w}_x} x_1 + (1 - \mu_M) \frac{w_{a,jx}}{\bar{w}_x} x_2 \\
\tilde{x}_3 &= (1 - \mu_m) \frac{w_{A,jx}}{\bar{w}_x} x_3 + \mu_m \frac{w_{a,jx}}{\bar{w}_x} x_4 \\
\tilde{x}_4 &= \mu_m \frac{w_{A,jx}}{\bar{w}_x} x_3 + (1 - \mu_m) \frac{w_{a,jx}}{\bar{w}_x} x_4 \\
\tilde{y}_1 &= (1 - \mu_M) \frac{w_{A,ky}}{\bar{w}_y} y_1 + \mu_M \frac{w_{a,ky}}{\bar{w}_y} y_2 \\
\tilde{y}_2 &= \mu_M \frac{w_{A,ky}}{\bar{w}_y} y_1 + (1 - \mu_M) \frac{w_{a,ky}}{\bar{w}_y} y_2 \\
\tilde{y}_3 &= (1 - \mu_m) \frac{w_{A,ky}}{\bar{w}_y} y_3 + \mu_m \frac{w_{a,ky}}{\bar{w}_y} y_4 \\
\tilde{y}_4 &= \mu_m \frac{w_{A,ky}}{\bar{w}_y} y_3 + (1 - \mu_m) \frac{w_{a,ky}}{\bar{w}_y} y_4,
\end{aligned} \tag{1}$$

where the  $\bar{w}_x$  and  $\bar{w}_y$  are the mean fitnesses in demes  $E_x$  and  $E_y$ , respectively. (For example,  $\bar{w}_x = w_{A,jx}x_1 + w_{a,jx}x_2 + w_{A,jx}x_3 + w_{a,jx}x_4$ .) The indices  $j$  and  $k$  denote the current temporal state within each deme ( $j, k \in \{1, 2\}$ ). The index  $j$  refers to deme  $E_x$ , while the index  $k$  refers to deme  $E_y$ .

After recombination and migration, the frequencies  $x'_i$  and  $y'_i$  ( $i \in \{1, 2, 3, 4\}$ ) at the start of the next generation can be written in terms of the post-switching frequencies  $\tilde{x}_i$  and  $\tilde{y}_i$  as

$$\begin{aligned}
x'_1 &= (1 - \nu) (\tilde{x}_1 - rD_{\tilde{x}}) + \nu (\tilde{y}_1 - rD_{\tilde{y}}) \\
x'_2 &= (1 - \nu) (\tilde{x}_2 + rD_{\tilde{x}}) + \nu (\tilde{y}_2 + rD_{\tilde{y}}) \\
x'_3 &= (1 - \nu) (\tilde{x}_3 + rD_{\tilde{x}}) + \nu (\tilde{y}_3 + rD_{\tilde{y}}) \\
x'_4 &= (1 - \nu) (\tilde{x}_4 - rD_{\tilde{x}}) + \nu (\tilde{y}_4 - rD_{\tilde{y}}) \\
y'_1 &= \nu (\tilde{x}_1 - rD_{\tilde{x}}) + (1 - \nu) (\tilde{y}_1 - rD_{\tilde{y}}) \\
y'_2 &= \nu (\tilde{x}_2 + rD_{\tilde{x}}) + (1 - \nu) (\tilde{y}_2 + rD_{\tilde{y}}) \\
y'_3 &= \nu (\tilde{x}_3 + rD_{\tilde{x}}) + (1 - \nu) (\tilde{y}_3 + rD_{\tilde{y}}) \\
y'_4 &= \nu (\tilde{x}_4 - rD_{\tilde{x}}) + (1 - \nu) (\tilde{y}_4 - rD_{\tilde{y}}),
\end{aligned} \tag{2}$$

where  $D_{\tilde{x}}$  and  $D_{\tilde{y}}$  are the linkage disequilibria in deme  $E_x$  and  $E_y$ , respectively ( $D_{\tilde{x}} = \tilde{x}_1\tilde{x}_4 - \tilde{x}_2\tilde{x}_3$  and

$$D_{\tilde{y}} = \tilde{y}_1\tilde{y}_4 - \tilde{y}_2\tilde{y}_3).$$

## Supplementary Figure Legends

**Figure S1. Invasion trials showing modifier frequency as a function of generation time.** The selection coefficients are all 0.1. Recombination and migration rates are 0.1. The environment switches deterministically in both demes every 10 generations. The stable switching rate in this case is 0.0271 and is the selected switching rate for the modifier allele  $m$ . The switching frequency determined by the wild-type allele  $M$  is shown by dot color. We chose wild-type rates both above and below the modifier rate. In all examples, the modifier spreads to fixation in both demes.

**Figure S2. Robustness of the result to different symmetric selection pressures.** All selection coefficients are equal and as presented in the legend. Recombination rate is 0.1. The expected time before an environmental change in both demes is 10 generations, and the environmental variability  $\psi$  (the variance of the gamma distribution divided by the square of its mean) is 0.1. The plotted curves represent a fit to the data using a generalized additive model with penalized cubic regression splines

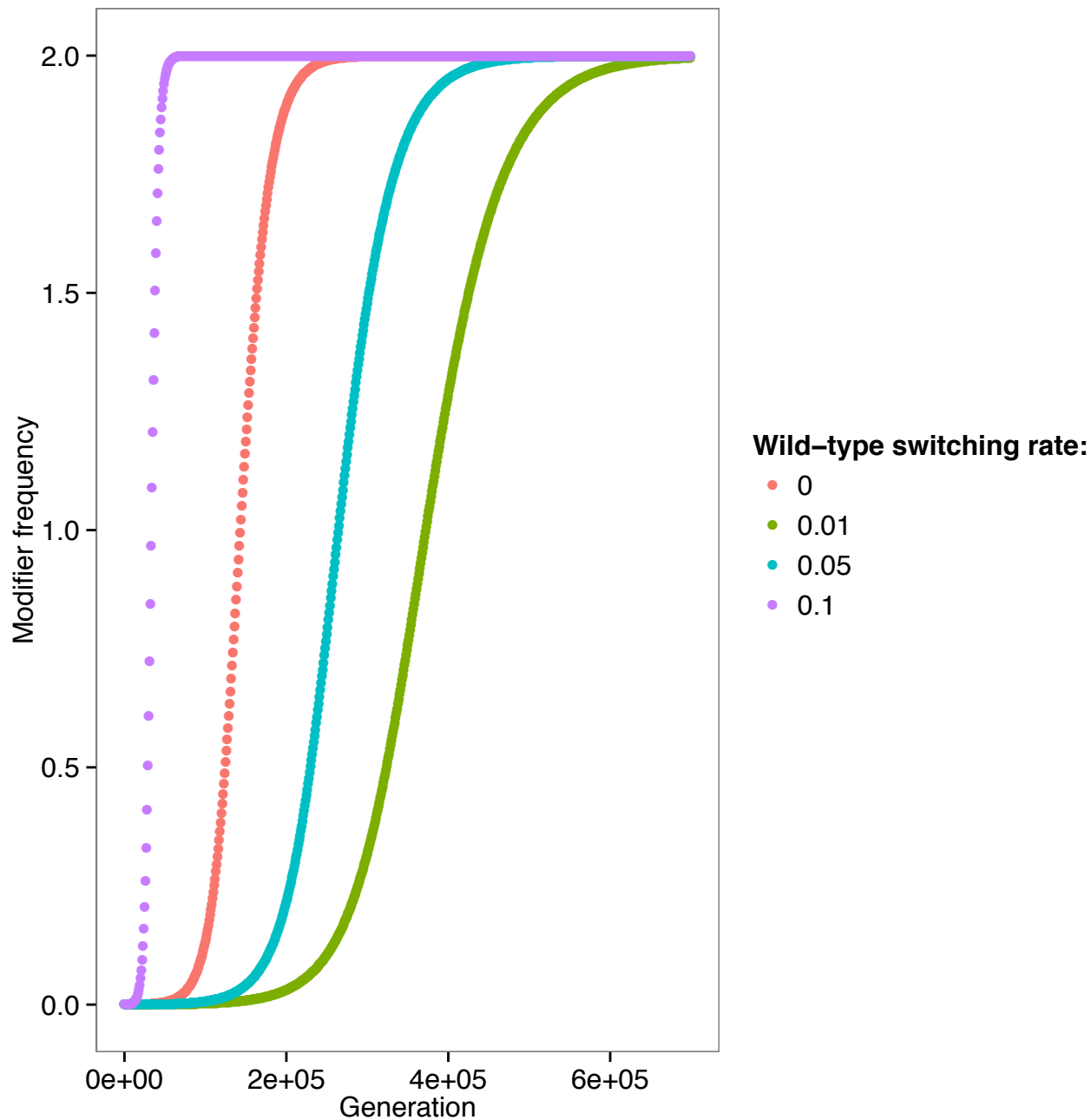
**Figure S3. Robustness of the symmetric selection results to different environmental mean waiting times.** The selection coefficients are all 0.1. Recombination rate is 0.1. The environmental variability  $\psi$  is 0.1. **Panel A:** The expected time before an environmental change is the same in both demes and presented in the legend. **Panel B:** The expected time before an environmental change is 10 generations in deme  $E_x$ . The expected time before an environmental change in deme  $E_x$  is represented by line color. The plotted curves represent a fit to the data using a generalized additive model with penalized cubic regression splines.

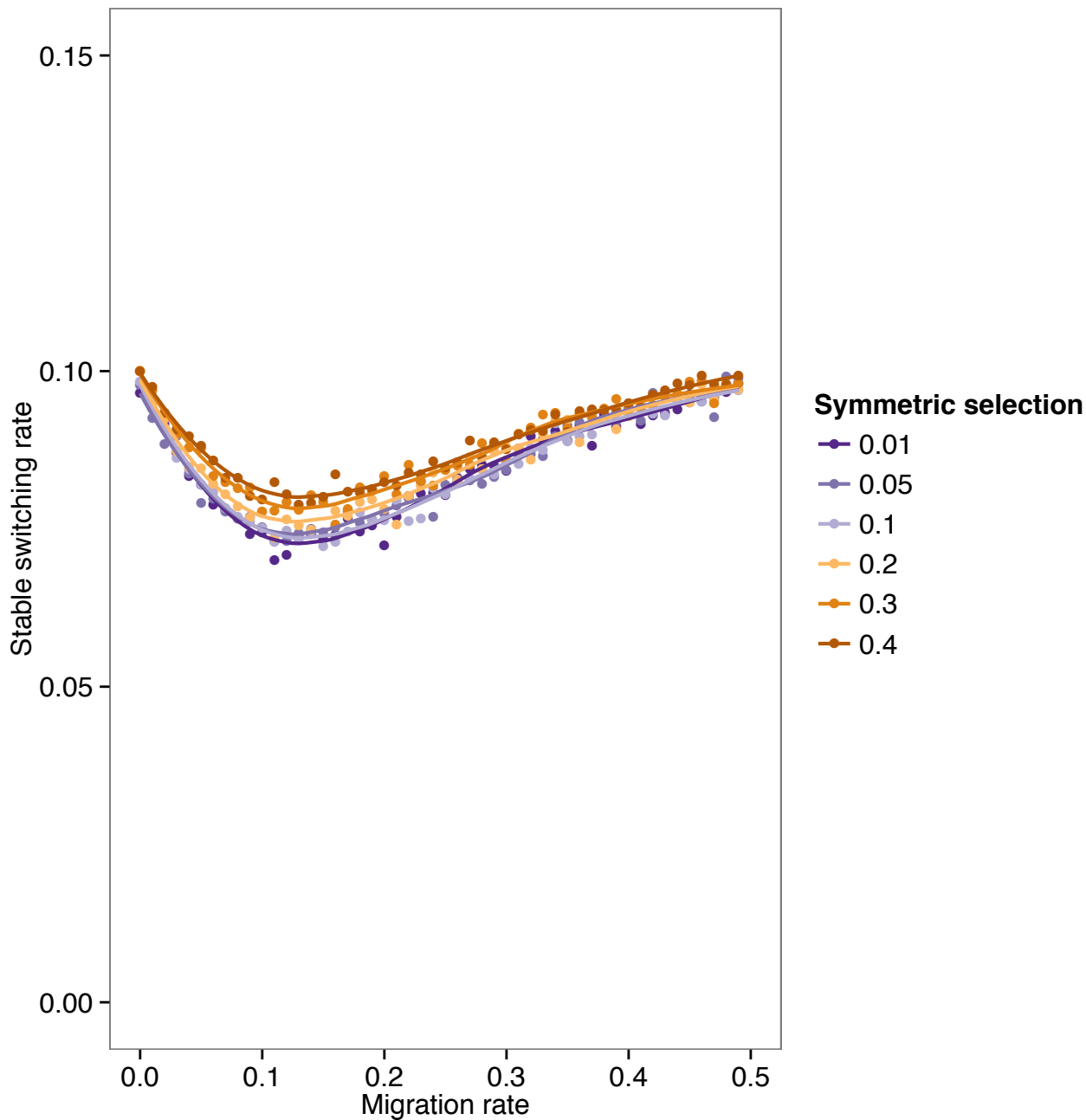
**Figure S4. The stable switching rate as a function of migration when selection strengths differ between demes.** The selection coefficients are  $s_1 = s_2 = 0.4$  and  $s_3 = s_4 = 0.1$ . Recombination rate is 0.1. The expected time before and environmental change in both demes is 10, and the environmental variability  $\psi$  is represented by line color. The plotted curves represent a fit to the data using a generalized additive model with penalized cubic regression splines.

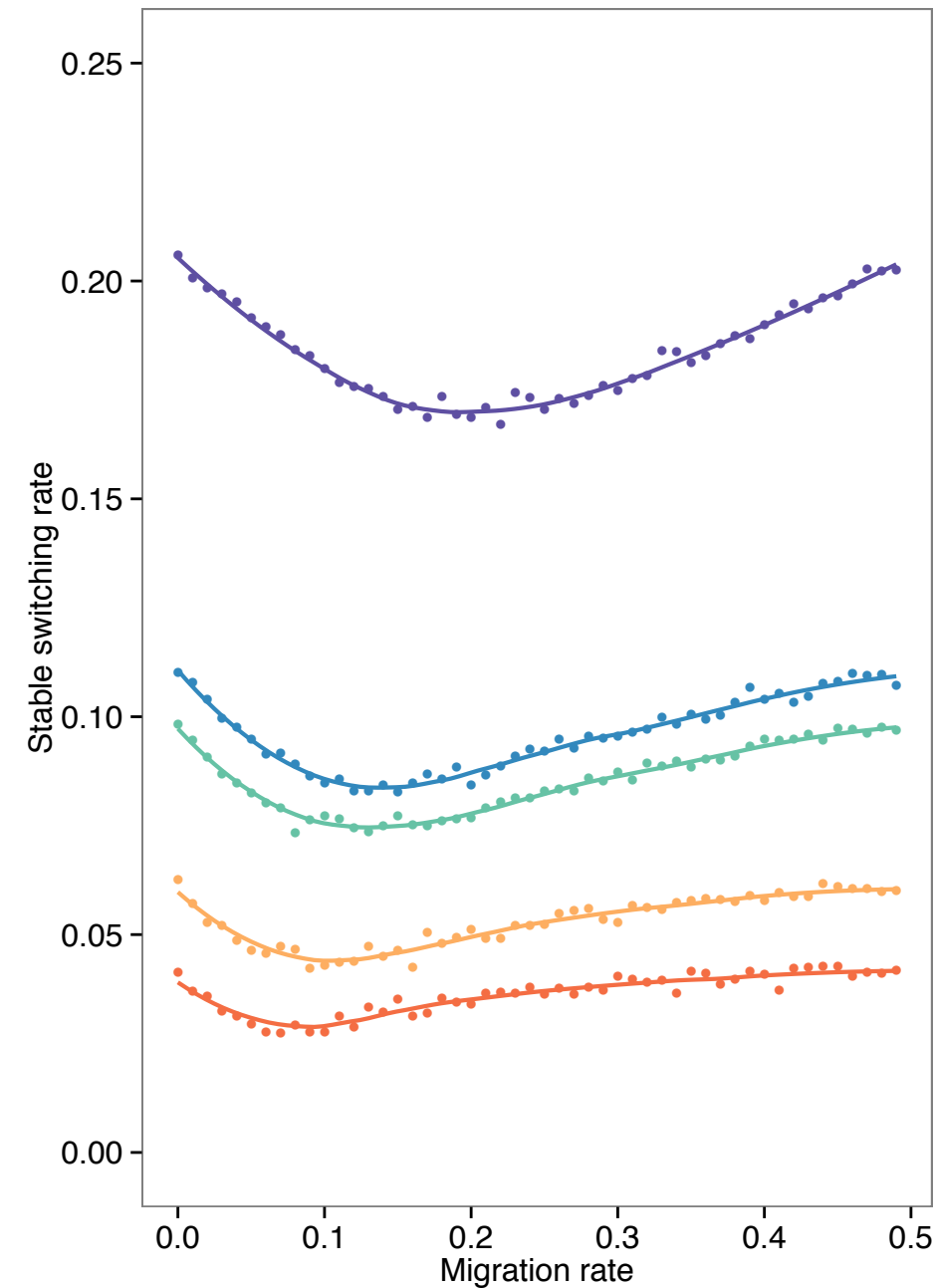
**Figure S5. Robustness of the asymmetric selection results to different environmental mean waiting times.** The selection coefficients are  $s_1 = s_3 = 0.4$  and  $s_2 = s_4 = 0.1$ . Recombination rate is 0.1. The environmental variability  $\psi$  is 0.1. **Panel A:** The expected time before an environmental change is the same in both demes and presented in the legend. **Panel B:** The expected time before an environmental change is 10 generations in deme  $E_x$ . The expected time before an environmental change

in deme  $E_x$  is represented by line color. The plotted curves represent a fit to the data using a generalized additive model with penalized cubic regression splines.

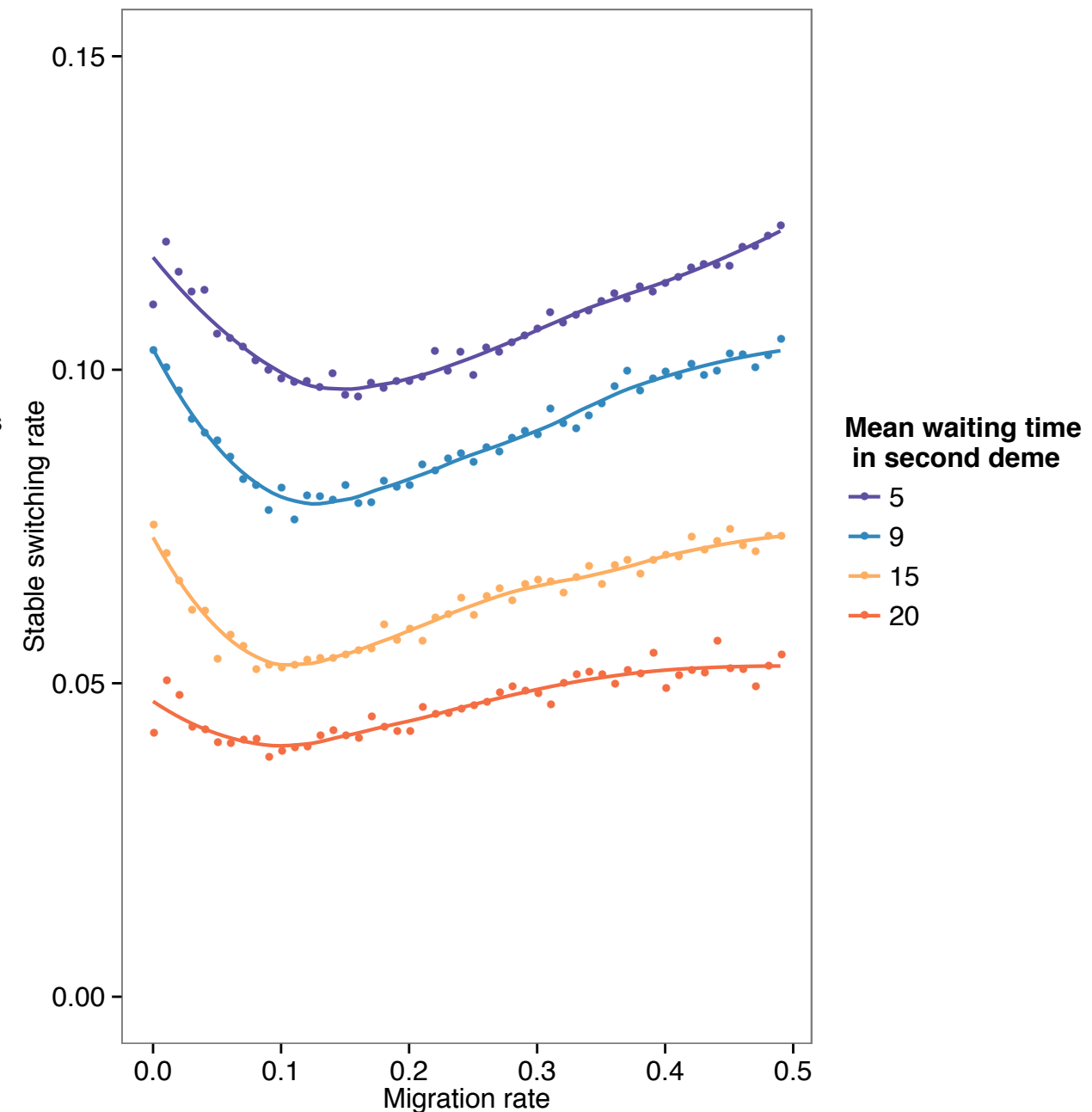
**Figure S6. Recombination and the stable switching rate.** The selection coefficients are all 0.1 and the environments switch with an expected period of 5 generations. The migration rate  $\nu = 0.05$ , and the environmental variability  $\psi$  is represented by line color. The plotted curves represent a fit to the data using a generalized additive model with penalized cubic regression splines.





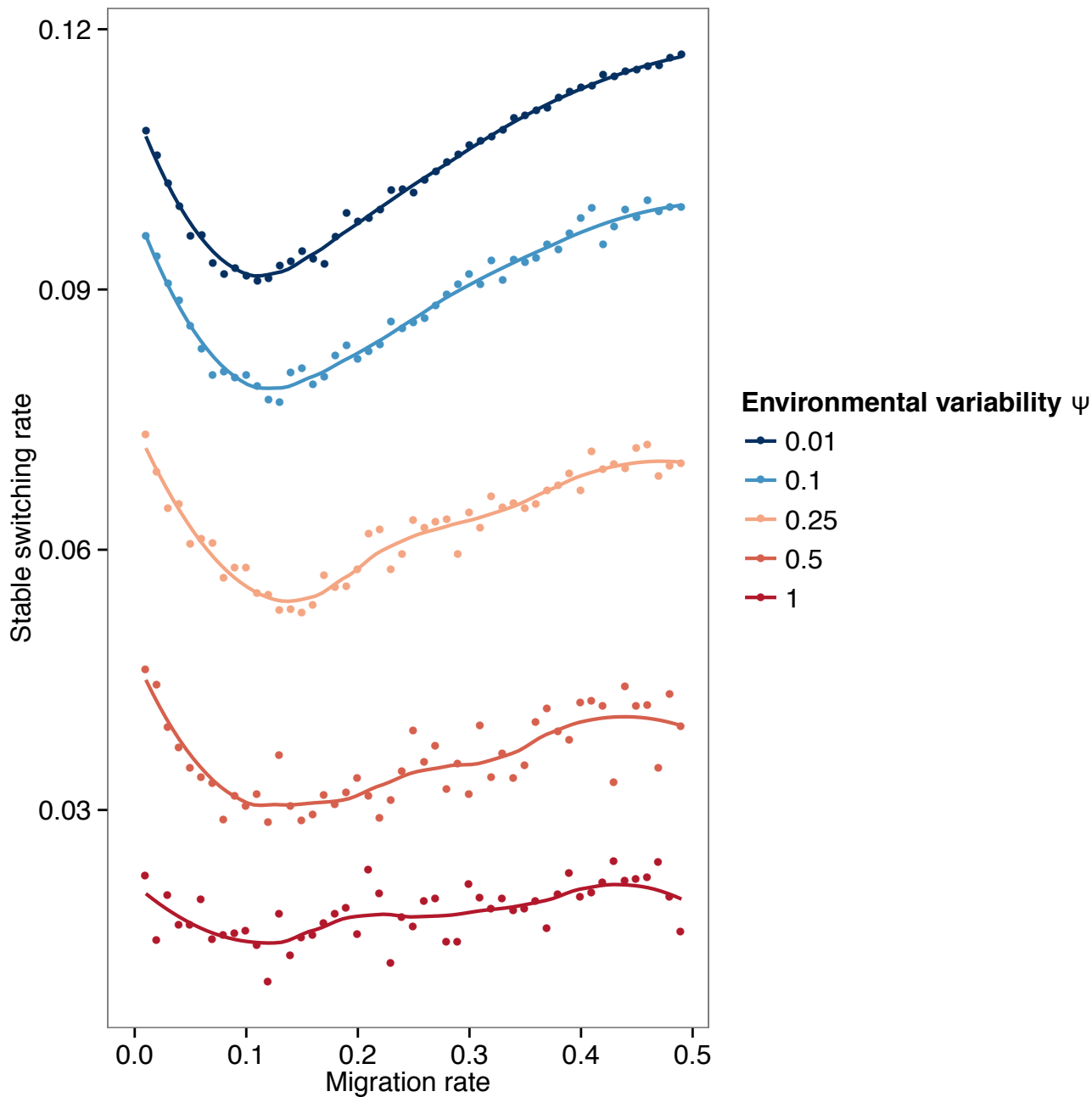


A

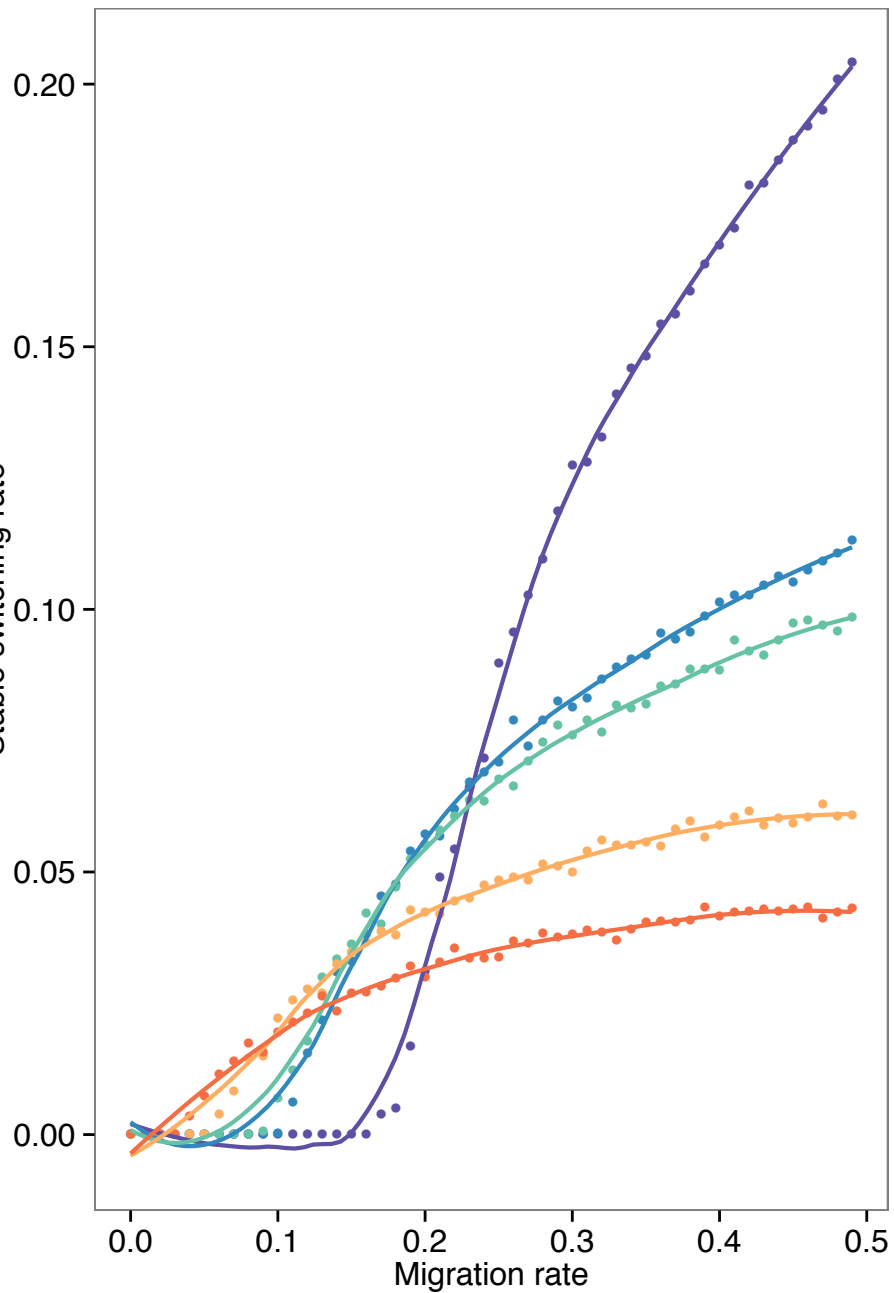


B



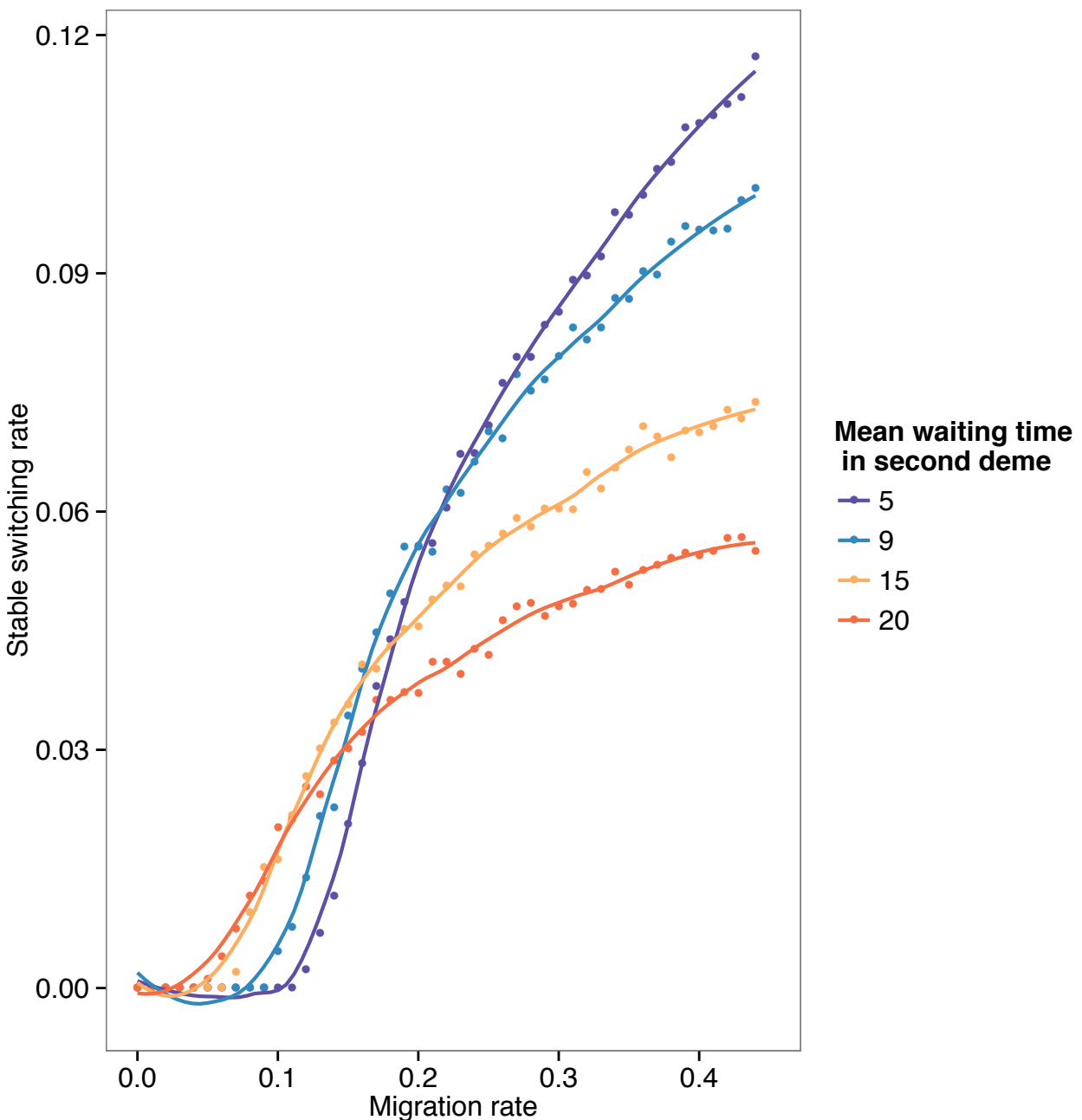


Stable switching rate



A

Stable switching rate



B

